#5

SEQUENCE LISTING

<110> Millennium Pharmaceuticals, Inc.
Rosana Kapeller-Libermann

<120> 23430, A NOVEL HUMAN UBIQUITIN HYDROLASE FAMILY MEMBER AND USES THEREFOR

<130> 38155-20024.00

<140> US 09/905,301
<141> 2001-07-13

<150> US 60/218,245
<151> 2000-07-14

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atc ctg gag ggc ctt gtg agt tcc tcg cat ccc ctg ccc ctc aag cgg      645
Ile Leu Glu Gly Leu Val Ser Ser Ser His Pro Leu Pro Leu Lys Arg
     5                  10                  15

gtg att gtg cgg aag gtg gtg gaa tcg gcg gag cac tgg cta gac gag      693
Val Ile Val Arg Lys Val Val Glu Ser Ala Glu His Trp Leu Asp Glu
 20                  25                  30                  35

gcg cag tgc gag gcc atg ttt gac ctg acg acc cgg ctc atc ctg gag      741
Ala Gln Cys Glu Ala Met Phe Asp Leu Thr Thr Arg Leu Ile Leu Glu
                 40                  45                  50

ggc cag gac cct ttc cag cgg cag gtg ggg cac cag gtg ctg gag gcc      789
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Gly Gln Asp Pro Phe Gln Arg Gln Val Gly His Gln Val Leu Glu Ala
             55                  60                  65

tac gca cga tac cac cgg cca gag ttc gag tcc ttc ttc aac aag acc      837
Tyr Ala Arg Tyr His Arg Pro Glu Phe Glu Ser Phe Phe Asn Lys Thr
         70                  75                  80

ttc gtg ttg ggc ctc ctt cat cag ggc tac cac tct ctg gac agg aag      885
Phe Val Leu Gly Leu Leu His Gln Gly Tyr His Ser Leu Asp Arg Lys
     85                  90                  95

gat gta gcc atc ctg gac tac att cac aac ggc ctg aag ctg att atg      933
Asp Val Ala Ile Leu Asp Tyr Ile His Asn Gly Leu Lys Leu Ile Met
100                 105                 110                 115

agc tgt ccg tcg gtg ctg gat ctc ttt agc ctc ctg cag gta gag gtg      981
Ser Cys Pro Ser Val Leu Asp Leu Phe Ser Leu Leu Gln Val Glu Val
                120                 125                 130

tta cgg atg gtg tgt gag agg ccg gag ccg cag ctc tgt gcc cga ctg     1029
Leu Arg Met Val Cys Glu Arg Pro Glu Pro Gln Leu Cys Ala Arg Leu
            135                 140                 145

agc gac ctt ctg acc gac ttt gtg caa tgc atc ccc aag ggg aaa ttg     1077
Ser Asp Leu Leu Thr Asp Phe Val Gln Cys Ile Pro Lys Gly Lys Leu
        150                 155                 160

tcc atc acg ttc tgt caa cag ctg gtt cga acg ata ggc cat ttc cag     1125
Ser Ile Thr Phe Cys Gln Gln Leu Val Arg Thr Ile Gly His Phe Gln
    165                 170                 175

tgc gtg tcc acc cag gaa aga gag ctg cgg gaa tat gtc tcc cag gtg     1173
Cys Val Ser Thr Gln Glu Arg Glu Leu Arg Glu Tyr Val Ser Gln Val
180                 185                 190                 195

aca aaa gtg agt aac ttg ctg cag aac atc tgg aag gcc gag cct gcc     1221
Thr Lys Val Ser Asn Leu Leu Gln Asn Ile Trp Lys Ala Glu Pro Ala
                200                 205                 210

aca cta ctg cct tcc ctg caa gaa gtt ttt gca agc atc tct tcc aca     1269
Thr Leu Leu Pro Ser Leu Gln Glu Val Phe Ala Ser Ile Ser Ser Thr
            215                 220                 225

gat gca tca ttt gaa cct tct gta gca ttg gca agc ctt gtg cag cat     1317
Asp Ala Ser Phe Glu Pro Ser Val Ala Leu Ala Ser Leu Val Gln His
        230                 235                 240

att cct ctt cag atg att aca gtt ctc atc agg agc ctt act acg gat     1365
Ile Pro Leu Gln Met Ile Thr Val Leu Ile Arg Ser Leu Thr Thr Asp
    245                 250                 255

cca aat gta aaa gat gca agt atg acc caa gcc ctt tgc aga atg att     1413
Pro Asn Val Lys Asp Ala Ser Met Thr Gln Ala Leu Cys Arg Met Ile
260                 265                 270                 275

gac tgg cta tcc tgg cca ttg gct cag cat gtg gat aca tgg gta att     1461
Asp Trp Leu Ser Trp Pro Leu Ala Gln His Val Asp Thr Trp Val Ile
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                280                 285                 290

gca ctc ctg aaa gga ctg gca gct gtc cag aag ttt act att ttg ata     1509
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            295                 300                 305

gat gtt act ttg ctg aaa ata gaa ctg gtt ttt aat cga ctt tgg ttt     1557
Asp Val Thr Leu Leu Lys Ile Glu Leu Val Phe Asn Arg Leu Trp Phe
        310                 315                 320

cct ctt gtg aga cct ggt gct ctt gca gtt ctt tct cac atg ctg ctt     1605
Pro Leu Val Arg Pro Gly Ala Leu Ala Val Leu Ser His Met Leu Leu
    325                 330                 335

agc ttt cag cat tct cca gag gcg ttc cat ttg att gtt cct cat gtg     1653
Ser Phe Gln His Ser Pro Glu Ala Phe His Leu Ile Val Pro His Val
340                 345                 350                 355

gtt aat ttg gtt cat tct ttc aaa aat gat ggt ctg cct tca agt aca     1701
Val Asn Leu Val His Ser Phe Lys Asn Asp Gly Leu Pro Ser Ser Thr
                360                 365                 370

gcc ttc tta gta caa tta aca gaa ttg ata cac tgt atg atg tat cat     1749
Ala Phe Leu Val Gln Leu Thr Glu Leu Ile His Cys Met Met Tyr His
            375                 380                 385

tat tct gga ttt cca gat ctc tat gaa cct att ctg gag gca ata aag     1797
Tyr Ser Gly Phe Pro Asp Leu Tyr Glu Pro Ile Leu Glu Ala Ile Lys
        390                 395                 400

gat ttt cct aag ccc agt gaa gag aag att aag tta att ctc aat caa     1845
Asp Phe Pro Lys Pro Ser Glu Glu Lys Ile Lys Leu Ile Leu Asn Gln
    405                 410                 415

agt gcc tgg act tct caa tcc aat tct ttg gcg tct tgc ttg tct aga     1893
Ser Ala Trp Thr Ser Gln Ser Asn Ser Leu Ala Ser Cys Leu Ser Arg
420                 425                 430                 435

ctt tct gga aaa tct gaa act ggg aaa act ggt ctt att aac cta gga     1941
Leu Ser Gly Lys Ser Glu Thr Gly Lys Thr Gly Leu Ile Asn Leu Gly
                440                 445                 450

aat aca tgt tat atg aac agt gtt ata caa gcc ttg ttt atg gcc aca     1989
Asn Thr Cys Tyr Met Asn Ser Val Ile Gln Ala Leu Phe Met Ala Thr
            455                 460                 465

gat ttc agg aga caa gta tta tct tta aat cta aat ggg tgc aat tca     2037
Asp Phe Arg Arg Gln Val Leu Ser Leu Asn Leu Asn Gly Cys Asn Ser
        470                 475                 480

tta atg aaa aaa tta cag cat ctt ttt gcc ttt ctg gcc cat aca cag     2085
Leu Met Lys Lys Leu Gln His Leu Phe Ala Phe Leu Ala His Thr Gln
    485                 490                 495

agg gaa gca tac gca cct cgg ata ttc ttt gag gct tcc aga cct cca     2133
Arg Glu Ala Tyr Ala Pro Arg Ile Phe Phe Glu Ala Ser Arg Pro Pro
500                 505                 510                 515
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tgg ttt act ccc aga tca cag caa gac tgt tct gaa tac ctc aga ttt     2181
Trp Phe Thr Pro Arg Ser Gln Gln Asp Cys Ser Glu Tyr Leu Arg Phe
                520                 525                 530

ctc ctt gac agg ctc cat gaa gaa gaa aag atc ttg aaa gtt cag gcc     2229
Leu Leu Asp Arg Leu His Glu Glu Glu Lys Ile Leu Lys Val Gln Ala
            535                 540                 545

tca cac aag cct tct gaa att ctg gaa tgc agt gaa act tct tta cag     2277
Ser His Lys Pro Ser Glu Ile Leu Glu Cys Ser Glu Thr Ser Leu Gln
        550                 555                 560

gaa gta gct agt aaa gca gca gta cta aca gag acc cct cgt aca agt     2325
Glu Val Ala Ser Lys Ala Ala Val Leu Thr Glu Thr Pro Arg Thr Ser
    565                 570                 575

gac ggt gag aag act tta ata gaa aaa atg ttt gga gga aaa cta cga     2373
Asp Gly Glu Lys Thr Leu Ile Glu Lys Met Phe Gly Gly Lys Leu Arg
580                 585                 590                 595

act cac ata cgt tgt ttg aac tgc agg agt acc tca caa aaa gtg gaa     2421
Thr His Ile Arg Cys Leu Asn Cys Arg Ser Thr Ser Gln Lys Val Glu
                600                 605                 610

gcc ttt aca gat ctt tcg ctt gcc ttt tgt cct tcc tct tct ttg gaa     2469
Ala Phe Thr Asp Leu Ser Leu Ala Phe Cys Pro Ser Ser Ser Leu Glu
            615                 620                 625

aac atg tct gtc caa gat cca gca tca tca ccc agt ata caa gat ggt     2517
Asn Met Ser Val Gln Asp Pro Ala Ser Ser Pro Ser Ile Gln Asp Gly
        630                 635                 640

ggt cta atg caa gcc tct gta ccc ggt cct tca gaa gaa cca gta gtt     2565
Gly Leu Met Gln Ala Ser Val Pro Gly Pro Ser Glu Glu Pro Val Val
    645                 650                 655

tat aat cca aca aca gct gcc ttc atc tgt gac tca ctt gtg aat gaa     2613
Tyr Asn Pro Thr Thr Ala Ala Phe Ile Cys Asp Ser Leu Val Asn Glu
660                 665                 670                 675

aaa acc ata ggc agt cct cct aat gag ttt tac tgt tct gaa aac act     2661
Lys Thr Ile Gly Ser Pro Pro Asn Glu Phe Tyr Cys Ser Glu Asn Thr
                680                 685                 690

tct gtc cct aac gaa tct aac aag att ctt gtt aat aaa gat gta cct     2709
Ser Val Pro Asn Glu Ser Asn Lys Ile Leu Val Asn Lys Asp Val Pro
            695                 700                 705

cag aaa cca gga ggt gaa acc aca cct tca gta act gac tta cta aat     2757
Gln Lys Pro Gly Gly Glu Thr Thr Pro Ser Val Thr Asp Leu Leu Asn
        710                 715                 720

tat ttt ttg gct cca gag att ctt act ggt gat aac caa tat tat tgt     2805
Tyr Phe Leu Ala Pro Glu Ile Leu Thr Gly Asp Asn Gln Tyr Tyr Cys
    725                 730                 735
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gaa aac tgt gcc tct ctg caa aat gct gag aaa act atg caa atc acg     2853
Glu Asn Cys Ala Ser Leu Gln Asn Ala Glu Lys Thr Met Gln Ile Thr
740                 745                 750                 755

gag gaa cct gaa tac ctt att ctt act ctc ctg aga ttt tca tat gat     2901
Glu Glu Pro Glu Tyr Leu Ile Leu Thr Leu Leu Arg Phe Ser Tyr Asp
                760                 765                 770

cag aag tat cat gtg aga agg aaa att tta gac aat gta tca ctg cca     2949
Gln Lys Tyr His Val Arg Arg Lys Ile Leu Asp Asn Val Ser Leu Pro
            775                 780                 785

ctg gtt ttg gag ttg cca gtt aaa aga att act tct ttc tct tca ttg     2997
Leu Val Leu Glu Leu Pro Val Lys Arg Ile Thr Ser Phe Ser Ser Leu
        790                 795                 800

tca gaa agt tgg tct gta gat gtt gac ttc act gat ctt agt gag aac     3045
Ser Glu Ser Trp Ser Val Asp Val Asp Phe Thr Asp Leu Ser Glu Asn
    805                 810                 815

ctt gct aaa aaa tta aag cct tca ggg act gat gaa gct tcc tgc aca     3093
Leu Ala Lys Lys Leu Lys Pro Ser Gly Thr Asp Glu Ala Ser Cys Thr
820                 825                 830                 835

aaa ttg gtg ccc tat cta tta agt tcc gtt gtg gtt cac tct ggt ata     3141
Lys Leu Val Pro Tyr Leu Leu Ser Ser Val Val Val His Ser Gly Ile
                840                 845                 850

tcc tct gaa agt ggg cat tac tat tct tat gcc aga aat atc aca agt     3189
Ser Ser Glu Ser Gly His Tyr Tyr Ser Tyr Ala Arg Asn Ile Thr Ser
            855                 860                 865

aca gac tct tca tat cag atg tac cac cag tct gag gct ctg gca tta     3237
Thr Asp Ser Ser Tyr Gln Met Tyr His Gln Ser Glu Ala Leu Ala Leu
        870                 875                 880

gca tcc tcc cag agt cat tta cta ggg aga gat agt ccc agt gca gtt     3285
Ala Ser Ser Gln Ser His Leu Leu Gly Arg Asp Ser Pro Ser Ala Val
    885                 890                 895

ttt gaa cag gat ttg gaa aat aag gaa atg tca aaa gaa tgg ttt tta     3333
Phe Glu Gln Asp Leu Glu Asn Lys Glu Met Ser Lys Glu Trp Phe Leu
900                 905                 910                 915

ttt aat gac agt aga gtg aca ttt act tca ttt cag tca gtc cag aaa     3381
Phe Asn Asp Ser Arg Val Thr Phe Thr Ser Phe Gln Ser Val Gln Lys
                920                 925                 930

att acg agc agg ttt cca aag gac aca gct tat gtg ctt ttg tat aaa     3429
Ile Thr Ser Arg Phe Pro Lys Asp Thr Ala Tyr Val Leu Leu Tyr Lys
            935                 940                 945

aaa cag cat agt act aat ggt tta agt ggt aat aac cca acc agt gga     3477
Lys Gln His Ser Thr Asn Gly Leu Ser Gly Asn Asn Pro Thr Ser Gly
        950                 955                 960

ctc tgg ata aat gga gac cca cct cta cag aaa gaa ctt atg gat gct     3525
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Leu Trp Ile Asn Gly Asp Pro Pro Leu Gln Lys Glu Leu Met Asp Ala
    965                 970                 975

ata aca aaa gac aat aaa cta tat tta cag gaa caa gag ttg aat gct     3573
Ile Thr Lys Asp Asn Lys Leu Tyr Leu Gln Glu Gln Glu Leu Asn Ala
 980                 985                 990                 995

cga gcc cgg gcc ctc caa gct gca tct gct tca tgt tca ttt cgg ccc     3621
Arg Ala Arg Ala Leu Gln Ala Ala Ser Ala Ser Cys Ser Phe Arg Pro
                1000                1005                1010

aat gga ttt gat gac aac gac cca cca gga agc tgt gga cca act ggt     3669
Asn Gly Phe Asp Asp Asn Asp Pro Pro Gly Ser Cys Gly Pro Thr Gly
            1015                1020                1025

gga ggg ggt gga gga gga ttt aat aca gtt ggc aga ctc gta ttt tga     3717
Gly Gly Gly Gly Gly Gly Phe Asn Thr Val Gly Arg Leu Val Phe  *
        1030                1035                1040

tcctgagaga gtccaaaatg cactggtcac gaaacgtcta atactatgac tgttaaaatg   3777
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tcagcatcac tgtgtctgta tttcaagtac aaatgttttt aaaaaggatt ctttatacat   4317
atgtgctgaa ttgattttaa ggaaagttgc atgatcctgt aggagcaaca tttttaccta   4377
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            20                  25                  30
Leu Asp Glu Ala Gln Cys Glu Ala Met Phe Asp Leu Thr Thr Arg Leu
        35                  40                  45
Ile Leu Glu Gly Gln Asp Pro Phe Gln Arg Gln Val Gly His Gln Val
    50                  55                  60
Leu Glu Ala Tyr Ala Arg Tyr His Arg Pro Glu Phe Glu Ser Phe Phe
65                  70                  75                  80
Asn Lys Thr Phe Val Leu Gly Leu Leu His Gln Gly Tyr His Ser Leu
                85                  90                  95
Asp Arg Lys Asp Val Ala Ile Leu Asp Tyr Ile His Asn Gly Leu Lys
            100                 105                 110
Leu Ile Met Ser Cys Pro Ser Val Leu Asp Leu Phe Ser Leu Leu Gln
        115                 120                 125
Val Glu Val Leu Arg Met Val Cys Glu Arg Pro Glu Pro Gln Leu Cys
    130                 135                 140
Ala Arg Leu Ser Asp Leu Leu Thr Asp Phe Val Gln Cys Ile Pro Lys
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145                 150                 155                 160
Gly Lys Leu Ser Ile Thr Phe Cys Gln Gln Leu Val Arg Thr Ile Gly
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His Phe Gln Cys Val Ser Thr Gln Glu Arg Glu Leu Arg Glu Tyr Val
            180                 185                 190
Ser Gln Val Thr Lys Val Ser Asn Leu Leu Gln Asn Ile Trp Lys Ala
        195                 200                 205
Glu Pro Ala Thr Leu Leu Pro Ser Leu Gln Glu Val Phe Ala Ser Ile
    210                 215                 220
Ser Ser Thr Asp Ala Ser Phe Glu Pro Ser Val Ala Leu Ala Ser Leu
225                 230                 235                 240
Val Gln His Ile Pro Leu Gln Met Ile Thr Val Leu Ile Arg Ser Leu
                245                 250                 255
Thr Thr Asp Pro Asn Val Lys Asp Ala Ser Met Thr Gln Ala Leu Cys
            260                 265                 270
Arg Met Ile Asp Trp Leu Ser Trp Pro Leu Ala Gln His Val Asp Thr
        275                 280                 285
Trp Val Ile Ala Leu Leu Lys Gly Leu Ala Ala Val Gln Lys Phe Thr
    290                 295                 300
Ile Leu Ile Asp Val Thr Leu Leu Lys Ile Glu Leu Val Phe Asn Arg
305                 310                 315                 320
Leu Trp Phe Pro Leu Val Arg Pro Gly Ala Leu Ala Val Leu Ser His
                325                 330                 335
Met Leu Leu Ser Phe Gln His Ser Pro Glu Ala Phe His Leu Ile Val
            340                 345                 350
Pro His Val Val Asn Leu Val His Ser Phe Lys Asn Asp Gly Leu Pro
        355                 360                 365
Ser Ser Thr Ala Phe Leu Val Gln Leu Thr Glu Leu Ile His Cys Met
    370                 375                 380
Met Tyr His Tyr Ser Gly Phe Pro Asp Leu Tyr Glu Pro Ile Leu Glu
385                 390                 395                 400
Ala Ile Lys Asp Phe Pro Lys Pro Ser Glu Glu Lys Ile Lys Leu Ile
                405                 410                 415
Leu Asn Gln Ser Ala Trp Thr Ser Gln Ser Asn Ser Leu Ala Ser Cys
            420                 425                 430
Leu Ser Arg Leu Ser Gly Lys Ser Glu Thr Gly Lys Thr Gly Leu Ile
        435                 440                 445
Asn Leu Gly Asn Thr Cys Tyr Met Asn Ser Val Ile Gln Ala Leu Phe
    450                 455                 460
Met Ala Thr Asp Phe Arg Arg Gln Val Leu Ser Leu Asn Leu Asn Gly
465                 470                 475                 480
Cys Asn Ser Leu Met Lys Lys Leu Gln His Leu Phe Ala Phe Leu Ala
                485                 490                 495
His Thr Gln Arg Glu Ala Tyr Ala Pro Arg Ile Phe Phe Glu Ala Ser
            500                 505                 510
Arg Pro Pro Trp Phe Thr Pro Arg Ser Gln Gln Asp Cys Ser Glu Tyr
        515                 520                 525
Leu Arg Phe Leu Leu Asp Arg Leu His Glu Glu Glu Lys Ile Leu Lys
    530                 535                 540
Val Gln Ala Ser His Lys Pro Ser Glu Ile Leu Glu Cys Ser Glu Thr
545                 550                 555                 560
Ser Leu Gln Glu Val Ala Ser Lys Ala Ala Val Leu Thr Glu Thr Pro
                565                 570                 575
Arg Thr Ser Asp Gly Glu Lys Thr Leu Ile Glu Lys Met Phe Gly Gly
            580                 585                 590
Lys Leu Arg Thr His Ile Arg Cys Leu Asn Cys Arg Ser Thr Ser Gln
        595                 600                 605
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Lys Val Glu Ala Phe Thr Asp Leu Ser Leu Ala Phe Cys Pro Ser Ser
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Ser Leu Glu Asn Met Ser Val Gln Asp Pro Ala Ser Ser Pro Ser Ile
625                 630                 635                 640
Gln Asp Gly Gly Leu Met Gln Ala Ser Val Pro Gly Pro Ser Glu Glu
                645                 650                 655
Pro Val Val Tyr Asn Pro Thr Thr Ala Ala Phe Ile Cys Asp Ser Leu
            660                 665                 670
Val Asn Glu Lys Thr Ile Gly Ser Pro Pro Asn Glu Phe Tyr Cys Ser
        675                 680                 685
Glu Asn Thr Ser Val Pro Asn Glu Ser Asn Lys Ile Leu Val Asn Lys
    690                 695                 700
Asp Val Pro Gln Lys Pro Gly Gly Glu Thr Thr Pro Ser Val Thr Asp
705                 710                 715                 720
Leu Leu Asn Tyr Phe Leu Ala Pro Glu Ile Leu Thr Gly Asp Asn Gln
                725                 730                 735
Tyr Tyr Cys Glu Asn Cys Ala Ser Leu Gln Asn Ala Glu Lys Thr Met
            740                 745                 750
Gln Ile Thr Glu Glu Pro Glu Tyr Leu Ile Leu Thr Leu Leu Arg Phe
        755                 760                 765
Ser Tyr Asp Gln Lys Tyr His Val Arg Arg Lys Ile Leu Asp Asn Val
    770                 775                 780
Ser Leu Pro Leu Val Leu Glu Leu Pro Val Lys Arg Ile Thr Ser Phe
785                 790                 795                 800
Ser Ser Leu Ser Glu Ser Trp Ser Val Asp Val Asp Phe Thr Asp Leu
                805                 810                 815
Ser Glu Asn Leu Ala Lys Lys Leu Lys Pro Ser Gly Thr Asp Glu Ala
            820                 825                 830
Ser Cys Thr Lys Leu Val Pro Tyr Leu Leu Ser Ser Val Val Val His
        835                 840                 845
Ser Gly Ile Ser Ser Glu Ser Gly His Tyr Tyr Ser Tyr Ala Arg Asn
    850                 855                 860
Ile Thr Ser Thr Asp Ser Ser Tyr Gln Met Tyr His Gln Ser Glu Ala
865                 870                 875                 880
Leu Ala Leu Ala Ser Ser Gln Ser His Leu Leu Gly Arg Asp Ser Pro
                885                 890                 895
Ser Ala Val Phe Glu Gln Asp Leu Glu Asn Lys Glu Met Ser Lys Glu
            900                 905                 910
Trp Phe Leu Phe Asn Asp Ser Arg Val Thr Phe Thr Ser Phe Gln Ser
        915                 920                 925
Val Gln Lys Ile Thr Ser Arg Phe Pro Lys Asp Thr Ala Tyr Val Leu
    930                 935                 940
Leu Tyr Lys Lys Gln His Ser Thr Asn Gly Leu Ser Gly Asn Asn Pro
945                 950                 955                 960
Thr Ser Gly Leu Trp Ile Asn Gly Asp Pro Pro Leu Gln Lys Glu Leu
                965                 970                 975
Met Asp Ala Ile Thr Lys Asp Asn Lys Leu Tyr Leu Gln Glu Gln Glu
            980                 985                 990
Leu Asn Ala Arg Ala Arg Ala Leu Gln Ala Ala Ser Ala Ser Cys Ser
        995                 1000                1005
Phe Arg Pro Asn Gly Phe Asp Asp Asn Asp Pro Pro Gly Ser Cys Gly
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<213> Artificial Sequence

<220>
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Gln Cys Leu Phe Ser Ile Pro Pro Leu Arg Asp Tyr Leu Leu Asp Ile
20 25 30

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<211> 69
<212> PRT
<213> Artificial Sequence

<220>
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Ser Leu Ser Gly Gly His Tyr Thr Ala Tyr Val Lys Lys Glu Asn Trp
20 25 30
Tyr Lys Phe Asp Asp Asp Lys Val Ser Arg Val Thr Glu Glu Glu Val
35 40 45
Leu Lys Glu Ser Gly Gly Glu Ser Gly Asp Thr Ser Ser Ala Tyr Ile
50 55 60
Leu Phe Tyr Glu Arg
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<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Consesnsus amino acid

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Lys Pro Glu Glu Leu Glu Gly Asp Asn Lys Tyr His Cys Glu Lys Cys
20 25 30
Lys Lys Lys Gln Asp Ala Thr Lys Gln Leu Thr Ile Lys Lys Leu Pro
35 40 45
Gln Val Leu Thr Ile His Leu Lys Arg Phe Glu Tyr Asn Glu Glu Arg
50 55 60
Phe Ser Ser Asn Lys Ile Asn Lys His Val Ser Phe Pro Leu Glu Thr
65 70 75 80
Leu Asp Leu

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<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<223> Signature pattern for conserved region

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<223> Xaa = Any Amino Acid

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            20   25   30
Ala Cys Val Xaa Leu Ile Val Met Ser Gln
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<211> 26
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Tyr Xaa Leu Xaa Ser Ala Gly Leu Ile Val Met Phe Thr Xaa Xaa His
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            20   25